

1/38

Amino Acid and nucleotide sequence of the murine OKT3 heavy chain  
variable region (Accession #A222621)

MERHWIFLLLSVTAGVHSQVLQSGAELARPGASVKMCKASVYTFTRYTMHWVKRPGQGLEWIGYINPSRGYTN  
YNQFKDKATLTIDKSSSTAYMQLSSLTSEDSAVYCYARYDDHYCLDYWGQGTTLTVSSAKTTAPSVYPLAPVCGD  
TTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSIKVD  
KKIEPRGPTIKPCPPCKCAPNLLGGPSVEIFPPKIKDVLMSLSPIVTCVWVDSEDDPDVQISWVFNNEVEVHTAQ  
TQTHREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTL  
TCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGSGYFMYSKLRVEKKNVERNSYSCSVVHEGLNHHHTKSFS  
RTPGK

ORIGIN

1 gaattccctt ctccacagac actgaaaact ctgactcaac atggaaaggc ctggatctt  
61 ttactcctg ttgtcagtaa ctgcaggtgt ccaactccag gtccagctgc agcagtctgg  
121 ggctgaactg gcaagacctg gggcctcagt gaagatgtcc tgcaaggctt ctggctacac  
181 ctttactagg tacacgatgc actgggtaaa acagaggcct ggacagggtc tggaatggat  
241 tggatacatt aatcctagcc gtggttatac taattacaat cagaagtcca aggacaaggc  
301 cacattgact acagacaaat cctccagcac agcctacatg caactgagca gcctgacatc  
361 tgaggactct gcagtctatt actgtgcaag atattatgat gatcattact gccttgacta  
421 ctggggccaa ggcaccactc tcacagtctc ctacagccaa acaacagccc catcggtcta  
481 tccactggcc cctgtgtgtg gagatacaac tggctcctcg gtgactctag gatgcctggt

FIG. 1A

2/38

541 caaggggttat ttccctgagc cagtacatt gacctgaac tctggatccc tgtccagtgg  
 601 tgtgcacacc ttccagctg tctgcagtc tgacctctac acctcagca gctcagtgac  
 661 tgtaacctcg agcacctgg ccagccagtc catcacctgc aatgtggccc acccggaag  
 721 cagcaccaag gtggacaaga aaattgagc cagaggggccc acaatcaagc cctgtcctcc  
 781 atgcaaatgc ccagcaccta acctcttggg tggaccatcc gtcttcattc tccctccaaa  
 841 gatcaaggat gtactcatga tctccctgag ccccatagtc acatgtgtgg tgggtgatgt  
 901 gagcgaggat gaccagatg tccagatcag ctggtttgtg acaaacgtgg aagtacacac  
 961 agctcagaca caaacccata gagaggatta caacagtact ctccgggtgg tcagtgcctt  
 1021 ccccatccag caccaggact gcatgagtgg caaggagttc aaatgcaagg tcaacaacaa  
 1081 agacctccca gcgcccatcg agagaacct ctcaaaaccc aaagggtcag taagagctcc  
 1141 acaggtatat gtcttgcttc caccagaaga agagatgact aagaaacagg tcaactctgac  
 1201 ctgcatggtc acagacttca tgcctgaaga catttacgtg gagtggacca acaacgggaa  
 1261 aacagagcta aactacaaga aactgaacc agtccctggac tctgatggtt cttacttcac  
 1321 gtacagcaag ctgagagtgg aaaagaaga ctgggtggaa agaaatagct actcctgttc  
 1381 agtgggtccac gaggtgtctg acaatcacca cagactaag agcttctccc ggactccggg  
 1441 taaatgagct cagcaccac aaaactctca ggtccaaaaga gacaccaca ctcatctcca  
 1501 tgcttccctt gtataaataa agcaccagc aatgcctggg accatgtaaa aaaaaaaaa  
 1561 aaaggaattc

FIG. 1A (Cont.)

3/38

Amino Acid and nucleotide sequence of the murine OKT3 light chain  
variable region (Accession #A22259)

MDFOVQIFSELLISASVVISRGQIVLTQSPAIMSAPGEKVTMTCSASSV\$YNNWYQQKSGTSPKRWIYD  
TSKLAGVPAHFRGSGTSYSLTISGMEAEADAATYYCQWSSNPFTFGSGTKLEINRADTAPTVISIFPPS  
SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSITLLTKDEYERHNSY  
TCEATHKTSTSPIVKSFNREK

## ORIGIN

1 gaattcccaa agacaaaatg gattttcaag tgcagatttt cagcttcctg  
ctaatcagtg  
61 cctcagtcac aatatccaga ggacaaaattg ttctcaccca gtctccagca  
atcatgtctg  
121 catctccagg ggagaaggtc accatgacct gcagtgccag ctcaagtga  
agttacatga  
181 actggtacca gcagaagtca ggcacctccc ccaaaagatg gatttatgac  
acatccaaac  
241 tggcttctgg agtccctgct cacttcaggg gcagtgggtc tgggacctct  
tactctctca  
301 caatcagcgg catggaggct gaagatgctg ccacttatta ctgccagcag  
tggagtagta  
361 accattcac gtccggctcg gggacaaaagt tggaaataaa ccgggctgat  
actgcaccaa  
421 ctgtatccat ctccccacca tccagtgagc agttaacatc tggagggtgcc  
tcagtcgtgt

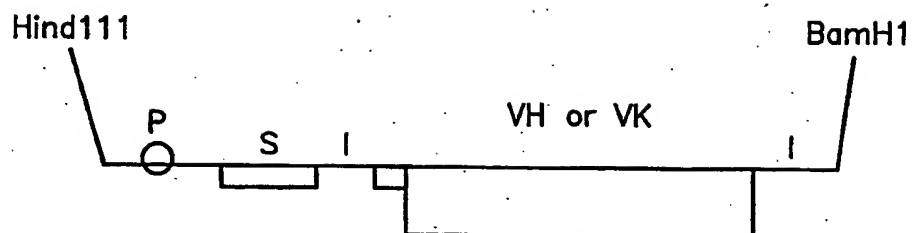
*FIG. 1B*

4/38

481 gcttcttgaa caactctac ccaaaagaca tcaatgtcaa gtggaagatt  
gatggcagtg  
541 aacgacaaaa tggcgtcctg aacagttgga ctgatcagga cagcaaagac  
agcacctaca  
601 gcatgagcag caccctcag ttgaccaagg acgagtatga acgacataac  
agctatacct  
661 gtgaggccac tcacaagaca tcaacttcac ccattgtcaa gagcttcaac  
aggaatgagt  
721 gttagagaca aaggtcctga gagccacca ccagctccca gctccatcct  
atcttccctt  
781 ctaaggctctt ggaggcttcc ccacaagcgc ttaccactgt tgcggtgctc  
taaacctcct  
841 cccacctcct tctctctcct ctccttttcc ttggctttta tcatgctaata  
attgcagaa  
901 aatattcaat aaagtgagtc ttgaccttga aaaaaaaaaaaa

*FIG. 1B (Cont.)*

5/38



P	Mouse heavy chain Ig promoter
S	Signal peptide sequence
I	Intron

*FIG. 2*

OKT3 VH gene construct.

Nucleic Acid and amino acid sequences of murine

Seq. ID No 1

HindIII

AAGCTTATGAATATGCAAAATCCTCTGAATCTACATGGTAAATATAGTTTGTCTATACCACAACAGAAACATGATCACAGTTCTCTACAGTTACTGACACAC  
 +-----+  
 TTCCGAATACTTATACGTTTAGGAGACTTAGATGTACCATTTATATCCAAACAGATATGGTGTCTTTTGTCTACTCTAGTGTCAAGAGATGTCATGACTCGTGTG

110

NcoI

AGGACCTCACCATGGGATGGAGCTGTATCATCTCTTGTGTAACAACAGCTACAGGTAGGGGCTCACAGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAA  
 +-----+  
 TCTGGAGTGTACCTACCTCGACATAGTAGGAGAAGAACCATCGTTGTCCGATGTCCATTTCCCGAGTGTATCGTCCGAACTCCAGACCTGTATATATACCCACTGTT

220

M G W S C I I L F L V A T A T  
 └──────────────────┘ Signal

Seq. ID No 2

PvuII

TGACATCCACTTTGCCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAGTGCACACAGTCTGGGGCTGAACCTCGCAAGACCTGGGGCTCAGTGAAGATGTCCTGCAAG  
 +-----+  
 ACTGTAGGTGAACGGAAGAGAGAGGTCTCCACAGGTGAGGTCCAGGTCCAGGTGTGTCAGACCCCGACTTGAGCGTTCTGGACCCCGGAGTCACTTCTACAGGACGTTCC

330

Seq. ID No 29 → G V H S Q V Q L Q Q S G A E L A R P G A S V K M S C K  
 └──────────┘ Signal └──────────┘ VH

FIG. 3

7/38

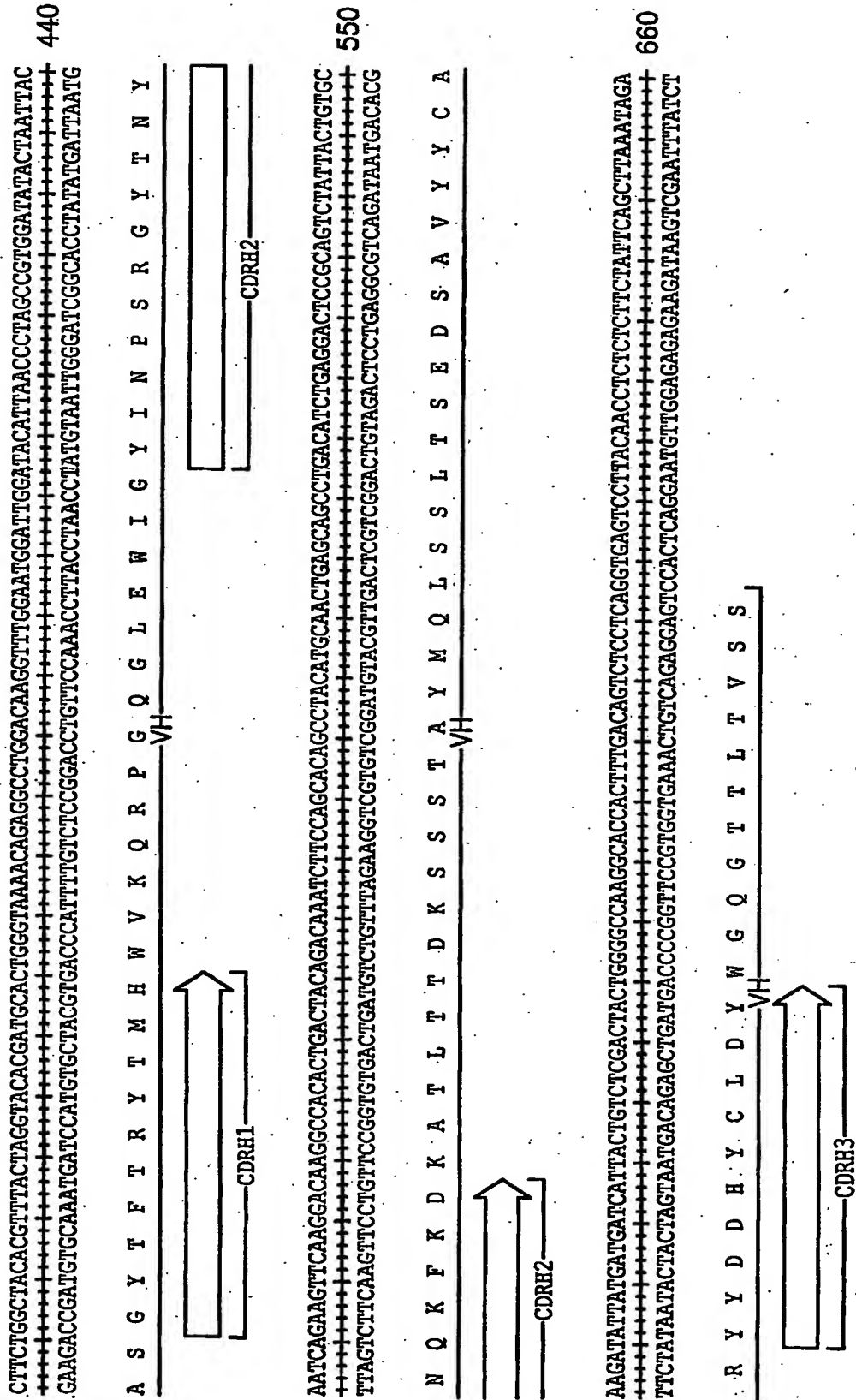


FIG. 3 (Cont.)

8/38

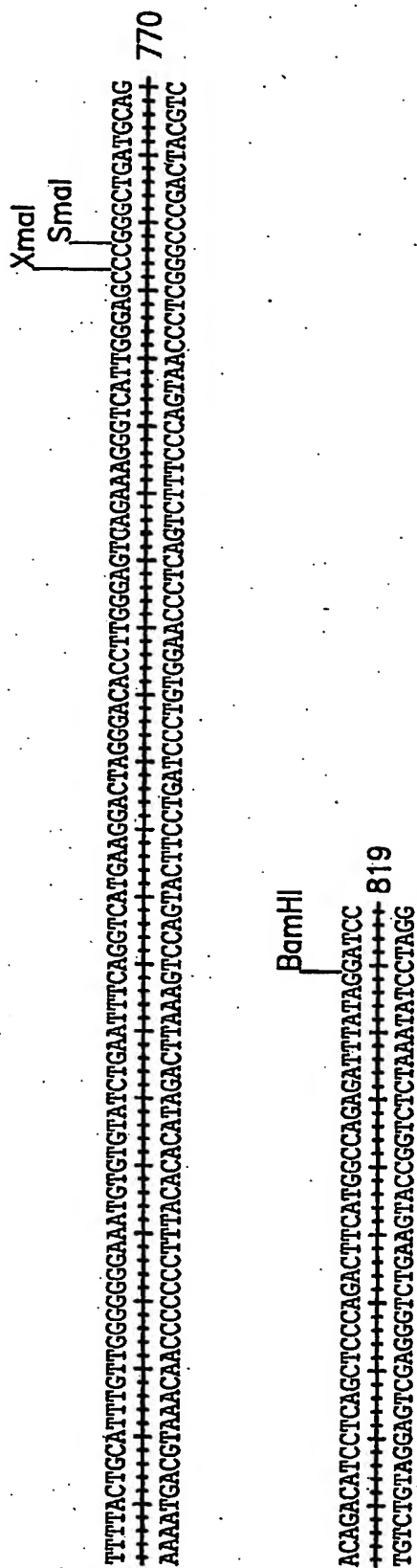


FIG. 3 (Cont.)



9/3.8

**OKT3 VL gene construct.**

## Nucleic acid and amino acid sequences of murine

Seq. ID. No 3

**Hindi**

AAGCTTATGAATATGCAAAATCCTCTGAATCATGTAATGTAATATAGGTTTGCTATATACCACAAACAGAAAAACATGAGATCACAGTTCCTCTACAGTTA  
 TTCCGAATACTTATACGTTTAGAGACCTTAGATGTACCAATTTATATCCAAACAGATATGGTGTGTTTGCTTTTGTACTCTAGTGTCAAGAGAGATGTCAAT

**Icon**

CTGAGCACACAGGACCTCAACCATGGGATGGAGCTGATCATCTCTCTTTGGTAGCAACAGCTACAGGTAAAGGGCTCACAGTAGCAGGCTTGAGGCTCG  
GACTCGTGTGTCCTGGAGTGATCCCTACCTCGACATAGTAGAGAGAAGAACCATCGTTTGTGCGATGTCCTTCCCGAGTTCATCGTCCGAACTCCAGAC

Seq. ID No 4 M G W S C I I L F L V A T A T  
Signal

GGCATATATATGGGTGACAATGACATCCACTTTGGCTTCTCTCCACAGGTGCCACTCCCAATTGTTCTCACCAGTCTCCAGCAATCATGTCTGCAT  
 CTCTATATATATACCCACTGTTACTGTAGTGAAACCGAAAGACAGAGGTGTCCACAGGTGAGGGTTTAAACAAGAGTGGGTCCAGAGGTCTGTTAGTACAGACGTA

Seq. ID No 30 → G V H S Q I V L T Q S P A I M S A  
Signal VK

BstE1

Kohl

TTCCAGGGG1AAAGGTCACTCATGCACTGCCAGCTCAAGTGTAACTACATGAACCTGGTACCGACAGTCAAGGCACCTCCCCCAAAAGATGGAT  
HANGTCCCTTTTCCAGTGGTACTGACGTACGGTCGAGTTCACATTCATGTACTTGACCATGGTCTCTTCAGTCCGTGGAGGGGCTTTTCTACCTA 400

**FIG. 4.**

10/38

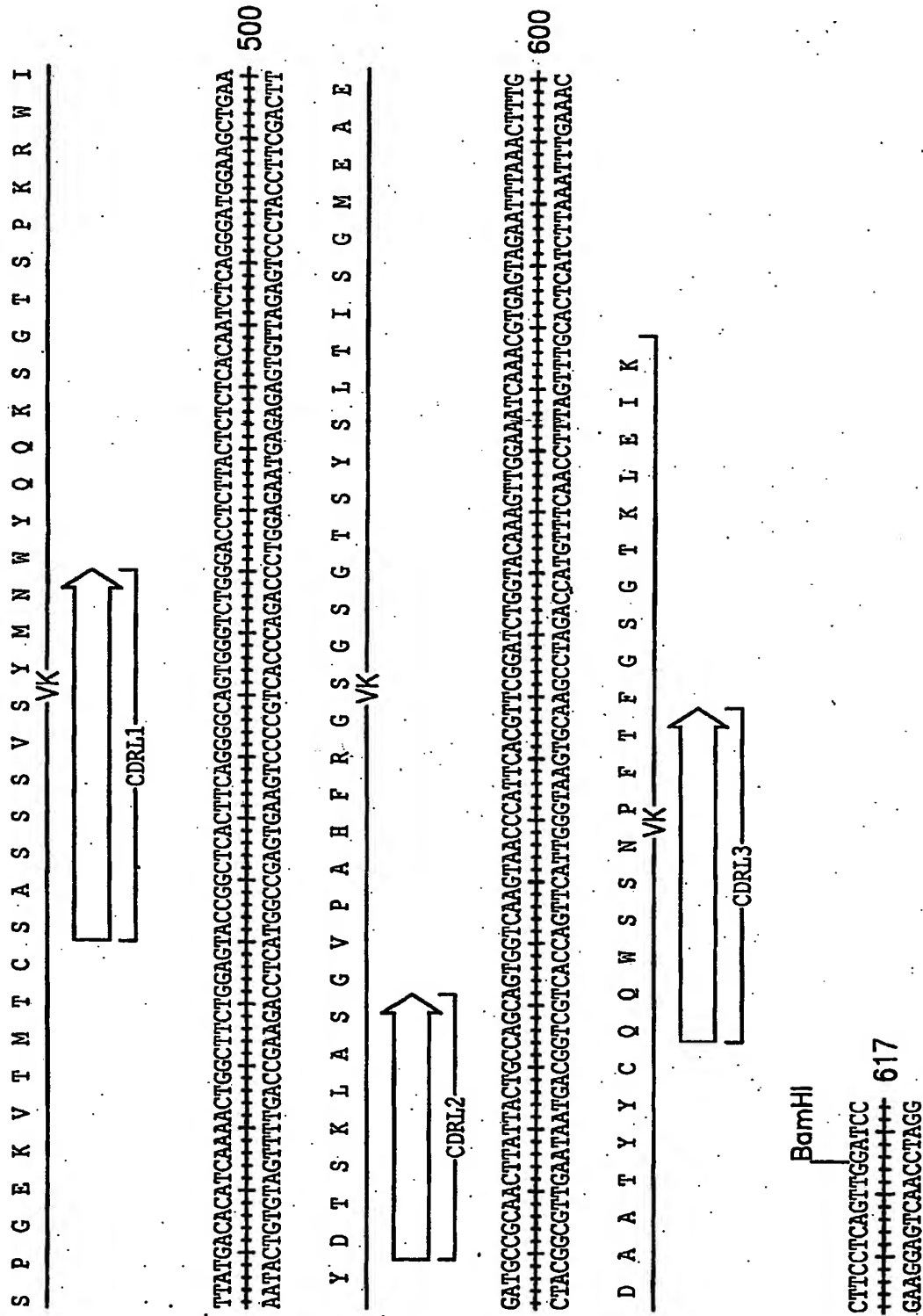
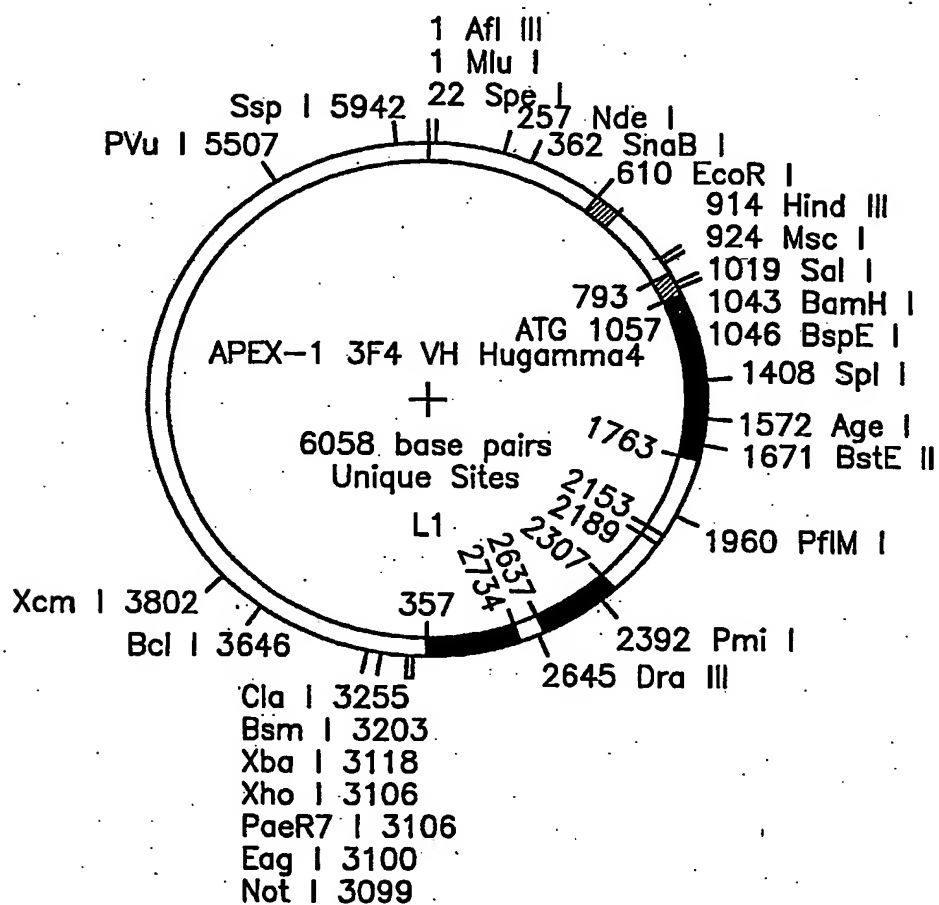


FIG. 4 (Cont.)

11/38

Schematic map of the vector Apex-1 3F4V<sub>H</sub>HuGamma4.**FIG. 5A**



ACTCTCCACTCCCTCAGTCAGACACCTTCTCTCTCCAGATCTGAGTAATCCCAATCTTCTCTGACAGATCCCAATATATGTCCTCCCATGCCCCATCATGCCAGTAAGCCACCCAGGCTCGCC 2210  
 Seq. ID No 31  $\xrightarrow{\text{E S K Y G P P C P S C P}}$  hG4Hinge  
 CTCAGCTCAAGCGGACAGGTGCCCTAGTAGCTGCTGCATCCAGGACAGGCCCCAGCGGGGTGCTGAGCGATCCACCTCCATCTCTCTCAGCACTGAGTTCCTGGGGGACCATCAGTCTTCT 2340  
 Seq. ID No 32  $\xrightarrow{\text{A P E F L G G P S V F L}}$  hG4CH2  
 FTCCCCCAAAACCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTACGTGCGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCACTGGTACGTGGCTGGAGGTGCAT 2470  
 F P P K P K D T L M I S R T P E V T C V V D V S Q E D P E V Q F N W Y V D G V E V H  
 hG4CH2  
 FTGCCAAGACAAAGCGCGGAGGAGCAGTTCAACAGCAGGTACCGTGTGGTACCGTCTCACCGTCTCGACCCAGGACTGGCTGACGGCAAGGAGTACAAAGTCAAGAGGCTCCAAAGGCTCC 2600  
 H A K T K P R E E Q F N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K G L  
 hG4CH2  
 Seq. ID No 33  
 FTCTCTCATCGAGAAACCATCTCCAAAGCCAAAGTGGGACCCACGGGGTGCAGGGCCACAGGACAGAGCCACGTTCGGCCACCCCTCTGCCCTGGAGTGACCGCTGTGCCAACCTCTGTCCCTA 2730  
 S S I E K T I S K A K  
 hG4CH2  
 3GGCAGCCCCGAGAGCCACAGGTGTACACCCCTGCCCCCATCCAGGAGGAGATGACCAAGAACAGTACGTGCTGCTGCTCAAGGCTTCTACCCCCAGGACATCGCGTGGAGTGGAGAG 2860  
 G Q P R E P Q V Y T L P P S Q E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S  
 hG4CH3  
 3ATGGCAGCCGGAGAACACTACAGACCCAGCTCCCGTGTGGACTCCGACGGTCTCTTCTCTACAGCAGGCTAACCGTGGACAGAGCAGGTGGCAGGAGGGAATCTTCTCATGCTCC 2990  
 N G Q P E N N Y K T T P P V L D S D G S F F L Y S R L T V D K S R W Q E G N V F S C S  
 hG4CH3  
 GTGATCATGAGGCTCTGCACAACCACTACACAGAGAGCTCTCCCTGTCTGTGGTAATGAGTCCAGGGCGGCAAGCCCCCGCTCCCATCCATCACACTGGCGGCGCGCTCGAGCATGCTATCT 3120  
 V M H E A L H N H Y T Q K S L S L G K  
 hG4CH3  
 AGAATGTTTATTGACGCTTATATGGTTACAAATAAGCAATAGCATCACAAATTTTACATGCAATTTTCTAGTCTTGTGGTTTGTCCAAACTCATATGTATCTTATCATGT 3250  
 CTGGATCGATCCCGGCATGTATCAACGCCATATTTCTATTTACAGTAGGACCTCTTCGTTGTGTAGTACCGCTGATTTCTAGGAAATAGTAGAGGACCTTGAACCTGTCTGTCATCAGCCATATAG 3380

13/38

SUBSTITUTE SHEET (RULE 26)

FIG. 5B (Cont.)

14/38

3510 GCGGCTGTTGACCTTACAAACAGGACAGTACTGACCAACCCATACACTCTCTGTAATACCATAGTTCGAGGGTGTCTCCGAACTCATTAACCTCCAAAGTCAGAGCTGTAATTTCCGCC 3510  
 3640 GTCAGAGGACGAGGGCTTCTCAGATATAATAGCTTCTGCGAGAGTCCGTAAGGTAGACACTTCAGCTTAATCCCTCGATGAGGTCTACTAGAAATAGTCAAGTGGGCTCCCAATTTTGAATAATTCAC 3640  
 3770 GACTTGATCAGCTTCAGACAGATGCGGAGGGCTCCACACAGTAATTTTCTCCGCACTCTTAATAATAGAAATAGTCAAGTCAAGTAAAGGAAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 3770  
 3900 GCTCTTTAATTAATGTTGCTAGGCAAGCCCTCCAGAGGGGCTGTTGTCAGAGGAAAGCAAAAGCCCTCCACCCAGGCTTGAATGTTTCCACCAATCATTAATGACAAACAGCTGTTTTTTTTT 3900  
 4030 GCTTAATTAAGCAGAGGCGGGGACCTTACTCTGGAGAAATAAGAGAGAGGCACTTCCAGAGGCACTTGTCAAAACAGGACTGCTTCTAATTTCTGTACACACTGCTCTGCCCC 4030  
 4160 GCTCACAAGGTCAGACACTCCATACCCCTTTAATAGCAGTTTGGAAACGGTGGGGTCTTACTCCGCCCATCCGCCCTAATCTCCGCCCATTTCCGCCCATTTCTCCGCCCATTTCTCCGCCCATTTCTCCGCCCAT 4160  
 4290 GCTTTTATTAATGAGGCGGCTCGGCTCTGAGCTATTTCCAGAGTGTGAGGAGCTTTTTGGAGGCTAGGCTTTTTGCAAAAGGAGCTCCAGCAAAAGGCCAGGAACCGTAAAAAG 4290  
 4420 GCGGCTGCTGGCGTTTTCATAGGCTCCGCCCTCCAGAGCATCAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGCACTAATAAGATPACAGGGGTTTTCCCTTGAAGCTCCC 4420  
 4550 GGTGCGCTCTCCTGTTCCGACCCCTGCGGCTTACCGGTAACCTGTCGCGCTTTCTCCCTTGGGAGGCTGGGCTTTCTCAATGCTCAAGCTGAGGTATCTCAAGTTCGGTGTAGTCTGCTGCTCA 4550  
 4680 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGACCGCTGGCGCTTATCCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 4680  
 4810 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 4810  
 4940 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 4940  
 5070 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 5070  
 5200 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 5200  
 5330 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 5330  
 5460 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 5460  
 5590 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 5590  
 5720 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 5720  
 5850 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 5850  
 5980 GGTGCGCTGCTGACGAAACCCCGCTTCAGCCGCTTACCGGTAACCTATGCTTGGTTCACACCCGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 5980

FIG. 5B (Cont.)

15/38

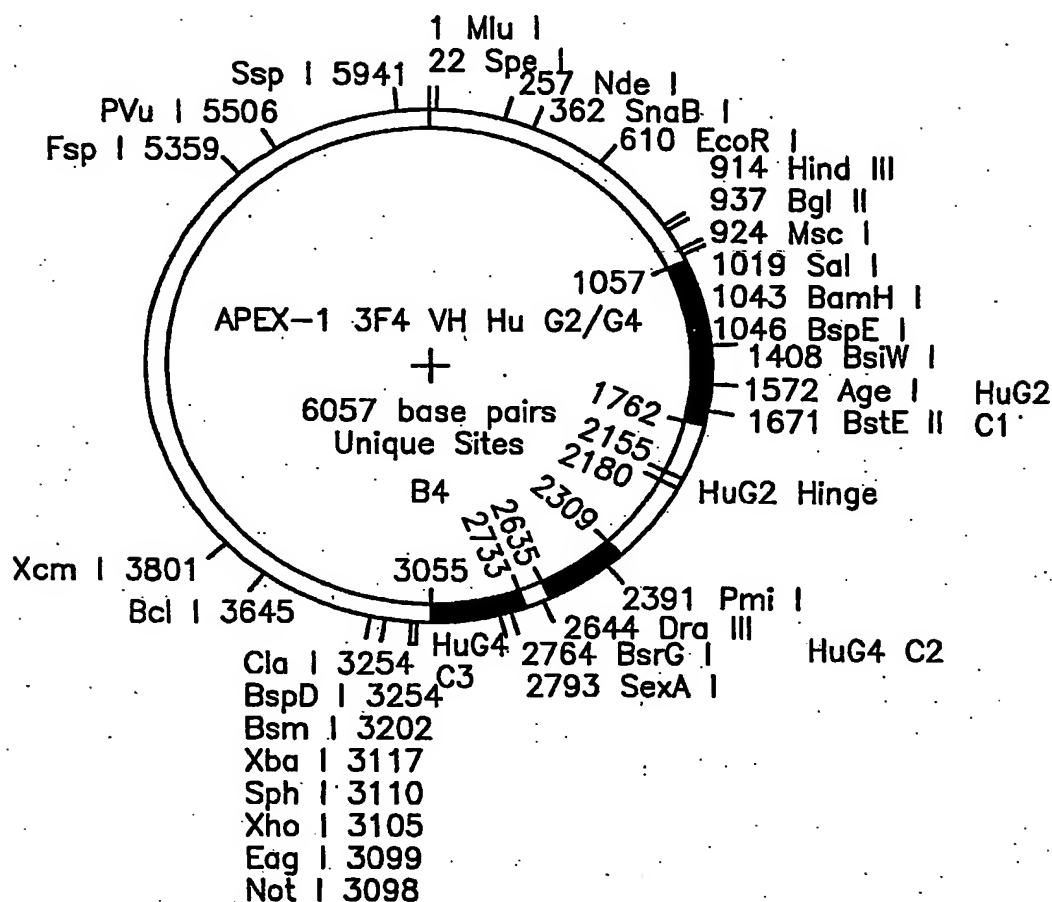
Schematic map of the vector Apex-1 3F4V<sub>H</sub>HuG2/G4.

FIG. 6A

Vector Sequence (APEX-13F4V<sub>H</sub>HuG2/G4)

ACGGTTGACATTGATTATTAATAGTAATCAATTAAGGGGTCAATTAGTTCATAGCCCATATATAGGAGTTCGGGTATCCGGTTACATTAAGGTAATAGGCCCGCCCTGGCTG 120  
 ACCGCCAACGACCCCGCCCATTCAGCTCAATATAGCAGTATGTTCCCATAGTAACCCCAATAGGAGCTTCCATTAGCTCAATGGGTGACATATTTACGTAACACGCCCACCTTGGC 240  
 AGTACATCAAGTGATCATATGCCAAGTAGCCCTATTGACGTCAATGACGGTAATAGCCCGCCCTGGCATATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACAT 360  
 CTACGATTAGTCAATCGCTATTACCATGCTGATGGGTTTGGCAGTACATCAATGCGGTGATAGCGTTTGGACTACGGGGATTCCAAAGTCTCCACCCCATTTGACGTCAATGGGAG 480  
 ATGTTTGGCACCAAAATCAACGGGACTTCCAAATGTCGTAACACTCCGCCCATTTGACGCAATAGGGCGGTAGGCTGTACGGTGGGAGTCTATATAGCAGAGCTCGTTTAGT 600  
 TAAACCTCAGAAATCTGTTGGGCTCGCGGTGATTAACAATCTTCCGGGTCTTCCAGTACTCTTTGGATCGGAACCCGTCGGCTCCGAAACGGTACTCCGCCACCGAGGGACCTGAGC 720  
 TAGTCCGCATCGACCGGATCGGAACCTCTCGACTGTTGGGTGAGTACTCCCTCTCAAAAGCGGGCATGACTTCTCGCTAAGATTGTCAAGTTCAGTTTCCAAACAGGAGGAGTATGATAT 840  
 TACCTGGCCCGGGTGATGCCCTTGAGGGTGGCGCGTCCATCTGCTCAGAAAAGACAATCTTTTGTGTCAGAGTGTGAGGCTTGAGATCTGGCCATACACACTTGAGTGA 960  
 CATGACATCCACTTTGCTTTCTCTCCACAGGTTCCACTCCAGGTCGAGGTCGACCGGCTGGTACCGAGCTCGGATCCGGACCATCATGAAGTGGAGCTGGGTATTCTC 1080  
 (Seq. ID No: 8) → M K W S W V I L ——— Signal ——— 16/38  
 TCCCTCTGTCAGTAATGCCGGGTCCACTCCAGGTTCCAGGTCAGGTCAGGTCGGGCTGAGTGGCAAGACCTTGGGCTCAGTGAAGTGTCTCTGCAAGGCTTCTGGCTACAAATTT 1200  
 L L L S V T A G V H S Q V Q V Q Q S G A E L A R P W A S V K L S C K A S G Y N F ——— Signal ——— 3F4Vh  
 ATAGTTACTGGATGCATGGGTAAACACAGAGGCTCGACAGGCTCTGGAATGGATTGGGGCTATTATCTCTGGAGATGGTGTATAGTACACTCAGAACTTCAGGGGCAAGGCCACA 1320  
 N S Y W M Q W V K Q R P G Q G L E W I G A I Y P G D G D T S Y T Q K F R G K A T ——— 3F4Vh  
 TGTGTCAGATAAATCTCCAGCACAGCTACATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGGGCTATATCTGTGCAAGACGTACGGTAGGAGGTACTTTGACTTGGGGC 1440  
 L T A D K S S S T A Y M Q L S S L A S E D S A V Y Y C A R R T V G G Y F D Y W G ——— 3F4Vh  
 CAAGGACCACTCTCAGAGTCTCTCAGCTCCACCAAGGGCCCATCCGCTCTCCCGCTGGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGCTGGTCAAGGAC 1560  
 Q G T T L T V S S A S T K G P S V F P L A P C S R S T S E S T A A L G C L V K D ——— 3F4Vh ——— G2G4CH1

SUBSTITUTE SHEET (RULE 26)

FIG. 6B



Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V  
G2G4CH1

P · S S N F G T Q T Y T C N V D H K P S N T K V D K T V  
 G2G4CH1  
 CCTCTCCAGCAACTTTCGGCACCCAGACCTACCTGCAACGTPAGATCAAGCCACGCAACACCAAGGTGGACACACACTTGGTCAGAGCCAGCTCAGGAGGAGGGTGCTGCTGGA 1800

1920  
 1925  
 1930  
 1935  
 1940  
 1945  
 1950  
 1955  
 1960  
 1965  
 1970  
 1975  
 1980  
 1985  
 1990  
 1995  
 2000  
 2005  
 2010  
 2015  
 2020  
 2025  
 2030  
 2035  
 2040  
 2045  
 2050  
 2055  
 2060  
 2065  
 2070  
 2075  
 2080  
 2085  
 2090  
 2095  
 2100  
 2105  
 2110  
 2115  
 2120  
 2125  
 2130  
 2135  
 2140  
 2145  
 2150  
 2155  
 2160  
 2165  
 2170  
 2175  
 2180  
 2185  
 2190  
 2195  
 2200  
 2205  
 2210  
 2215  
 2220  
 2225  
 2230  
 2235  
 2240  
 2245  
 2250  
 2255  
 2260  
 2265  
 2270  
 2275  
 2280  
 2285  
 2290  
 2295  
 2300  
 2305  
 2310  
 2315  
 2320  
 2325  
 2330  
 2335  
 2340  
 2345  
 2350  
 2355  
 2360  
 2365  
 2370  
 2375  
 2380  
 2385  
 2390  
 2395  
 2400  
 2405  
 2410  
 2415  
 2420  
 2425  
 2430  
 2435  
 2440  
 2445  
 2450  
 2455  
 2460  
 2465  
 2470  
 2475  
 2480  
 2485  
 2490  
 2495  
 2500  
 2505  
 2510  
 2515  
 2520  
 2525  
 2530  
 2535  
 2540  
 2545  
 2550  
 2555  
 2560  
 2565  
 2570  
 2575  
 2580  
 2585  
 2590  
 2595  
 2600  
 2605  
 2610  
 2615  
 2620  
 2625  
 2630  
 2635  
 2640  
 2645  
 2650  
 2655  
 2660  
 2665  
 2670  
 2675  
 2680  
 2685  
 2690  
 2695  
 2700  
 2705  
 2710  
 2715  
 2720  
 2725  
 2730  
 2735  
 2740  
 2745  
 2750  
 2755  
 2760  
 2765  
 2770  
 2775  
 2780  
 2785  
 2790  
 2795  
 2800  
 2805  
 2810  
 2815  
 2820  
 2825  
 2830  
 2835  
 2840  
 2845  
 2850  
 2855  
 2860  
 2865  
 2870  
 2875  
 2880  
 2885  
 2890  
 2895  
 2900  
 2905  
 2910  
 2915  
 2920  
 2925  
 2930  
 2935  
 2940  
 2945  
 2950  
 2955  
 2960  
 2965  
 2970  
 2975  
 2980  
 2985  
 2990  
 2995  
 3000  
 3005  
 3010  
 3015  
 3020  
 3025  
 3030  
 3035  
 3040  
 3045  
 3050  
 3055  
 3060  
 3065  
 3070  
 3075  
 3080  
 3085  
 3090  
 3095  
 3100  
 3105  
 3110  
 3115  
 3120  
 3125  
 3130  
 3135  
 3140  
 3145  
 3150  
 3155  
 3160  
 3165  
 3170  
 3175  
 3180  
 3185  
 3190  
 3195  
 3200  
 3205  
 3210  
 3215  
 3220  
 3225  
 3230  
 3235  
 3240  
 3245  
 3250  
 3255  
 3260  
 3265  
 3270  
 3275  
 3280  
 3285  
 3290  
 3295  
 3300  
 3305  
 3310  
 3315  
 3320  
 3325  
 3330  
 3335  
 3340  
 3345  
 3350  
 3355  
 3360  
 3365  
 3370  
 3375  
 3380  
 3385  
 3390  
 3395  
 3400  
 3405  
 3410  
 3415  
 3420  
 3425  
 3430  
 3435  
 3440  
 3445  
 3450  
 3455  
 3460  
 3465  
 3470  
 3475  
 3480  
 3485  
 3490  
 3495  
 3500  
 3505  
 3510  
 3515  
 3520  
 3525  
 3530  
 3535  
 3540  
 3545  
 3550  
 3555  
 3560  
 3565  
 3570  
 3575  
 3580  
 3585  
 3590  
 3595  
 3600  
 3605  
 3610  
 3615  
 3620  
 3625  
 3630  
 3635  
 3640  
 3645  
 3650  
 3655  
 3660  
 3665  
 3670  
 3675  
 3680  
 3685  
 3690  
 3695  
 3700  
 3705  
 3710  
 3715  
 3720  
 3725  
 3730  
 3735  
 3740  
 3745  
 3750  
 3755  
 3760  
 3765  
 3770  
 3775  
 3780  
 3785  
 3790  
 3795  
 3800  
 3805  
 3810  
 3815  
 3820  
 3825  
 3830  
 3835  
 3840  
 3845  
 3850  
 3855  
 3860  
 3865  
 3870  
 3875  
 3880  
 3885  
 3890  
 3895  
 3900  
 3905  
 3910  
 3915  
 3920  
 3925  
 3930  
 3935  
 3940  
 3945  
 3950  
 3955  
 3960  
 3965  
 3970  
 3975  
 3980  
 3985  
 3990  
 3995  
 4000  
 4005  
 4010  
 4015  
 4020  
 4025  
 4030  
 4035  
 4040  
 4045  
 4050  
 4055  
 4060  
 4065  
 4070  
 4075  
 4080  
 4085  
 4090  
 4095  
 4100  
 4105  
 4110  
 4115  
 4120  
 4125  
 4130  
 4135  
 4140  
 4145  
 4150  
 4155  
 4160  
 4165  
 4170  
 4175  
 4180  
 4185  
 4190

17/38  
Hinge-  
TATCTTGTGTGAGTGGCCACCGTGGCCAGGTAAAGCCAGCCAGCCCTCGCCCTCCAGCTCAAGGGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGACAGGCCCCAGCTGGTGCT 2280

Seq. ID No: 35) → A P P V A G P S V F L F P P P K P K D T L M I S R T P P E V T C V  
G2G4CH2

5' TGTGGTGGACGTGAGCCAGGAGACACCCGAGGTCACGTTCAACTGTGTACGTGGATGCGTGTGAGGTGCATATGCCAAGACAAAGCCCGGGGAGGACGTTCAACAGCAGCTACCGTGTG 2520  
A V V D V S Q E D P E V Q F F N W Y V D G V E V H N A K T K P R E E Q F N S T Y R V  
G2G4CH2

TCAGCGTCTCACCGTCTCGACCCAGGACTGGCTGAACGGCAAGGAGTACAATGTCAGGTCTCCACAAAGGCTCCCGTCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGG 2640

V S V L T V L H Q D W L N G K E Y K C K V S N K G L P S S I E K T I S K A K

G2G4CH2

**FIG. 6B (Cont.)**

18/38

**SUBSTITUTE SHEET (RULE 26)**

**FIG. 6B (Cont.)**

19/38

2 CTGCGCGTTACGGGATACTGTGTCGGCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGTTAGGTCTGCTCGCTCCCAAGCTGGCGTGTG 4560

3 TACACGAACCCCGCTTACAGCCCGGACCGCTTACCGGTAACTATCGTCTTGAGTCCAAACCCGGTAACACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCA 4680

4 GAGCAGGATGTAGGCGGTGTACAGAGTCTTGAAGTGTGGCTTAACACACAGTGTCTGCTGAAGCAGGTACCTTCGGAAGAAAGAG 4800

5 TTGGTAGTCTTTGATCCGGCAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTTCGAACGACGACATTAACGCGCAGAAAAAGGATCTCAAGAAAGATCCCTTTGATCTTTTCTPACGG 4920

6 GCTGTGACCTCATGTGAGACGAAACTCAGCTTAAGGATTTTGGTCATGAGATTATCAAAAGGATCTTCACTAGATCTTTTAAATTAATAAATGAAGTCTTTAAATCAATCTTAAAGTA 5040

7 TATATGAGTAATAACTGTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGCATCTGTCTATTTTGGTTTCATCCATAGTTTGCCTGACTCCCGCTGCTGTAGATACTACGA 5160

8 TACGGGAGGGCTTACCAATCTGGCCCCAGTGTGCAATGATACCGGAGACCCACGCTCACCGGCTCCAGATTATACGCAATTAACACGACCCAGCGGAGAGGCCGAGCGCAGAGAGTGGTC 5280

9 TCGCAACTTATACGCGCTCCATCCAGTCTAATTAATGTTCGGGGAAGCTACAGTAAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTTGGCCATTGCTACAGGCATCGTGGTGTCCAC 5400

10 SCTGCTGCTTTGGTATGGCTTCAATTCAGCTCCGGTCCCAACGATCAAGGGAGTTACATGATCCCGCATGTTGTGTGCAAAAAAGCGGTTAGTCTCTTCGGTCTCTCCGATCGTGTGCAGAA 5520

11 TTAAGTTGCCCGCAGTGTATCATCTCATGTGTTATGCGACGACTGCATTAATTTCTTTACTGTGCATGCCATCCGTAAGATGCTTTTCTGTGACTGCTGTGAGTACTCAACCAAGTCAATCTTGAG 5640

12 TATAGTGTATGCGCGGACCGAGTTGCTCTTGGCCCGGCTCAATACCGGATAATACCGCGCCACATACGAGAACTTTPAAAAAGTCTCATCATTTGGAAAAAGGTTCTTTCGGGCGGAAAACTCT 5760

13 TACAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCACTCTGTGCACCCCAACTGATCTTTCAGCATCTTTTACTTTTCCAGCGCTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATG 5880

14 TCGCAAAAAAGGGAATAAGGCGCACCGGAATATGTGAATACTCATPACTCTTCTCTTTTCAATATTAATGAGCAATTTATCAGGGTTATGTCTCATGAGCGGATACATATTTGAATGTA 6000

TTTAGAAAAATAACAAATAGGGGTTCGGGCACATTTCCCCGAAAAAGTGCCACCTG 6057

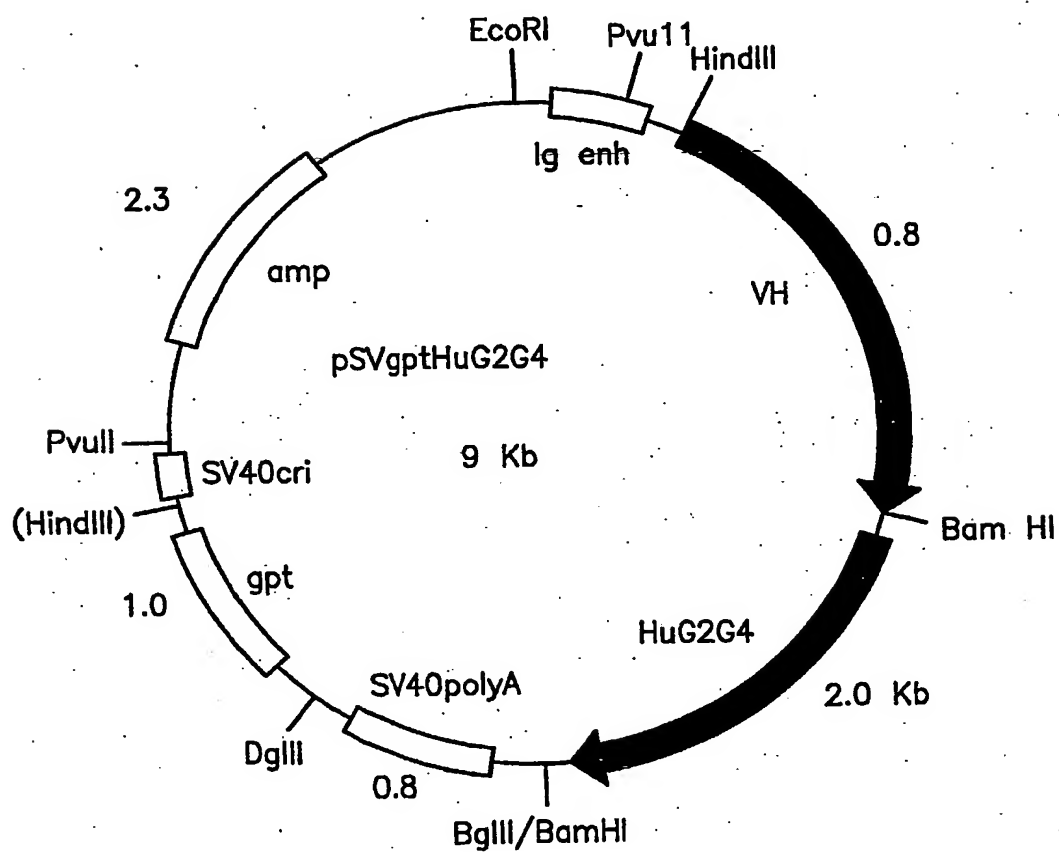
SUBSTITUTE SHEET (RULE 26)

**FIG. 6B (Cont.)**

6057

20/38

Map of the heavy chain expression vector pSVgptHuG2/G4 used in



**FIG. 7**

SUBSTITUTE SHEET (RULE 26)

21/38

(Seq. ID No. 9)

5' untranslated  
intron from  
native IgG4

Bam HI

GGATCCTCTAGATTGAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTGGG  
GGCAGGGAGGGGGCTAAGGTGACGCAGGTGGCGCCAGCCAGGTGCACACCC  
AATGCCCATGAGCCCAGACACTGGACCCTGCATGGACCATCGCGGATAGACA  
AGAACCGAGGGGCTCTGCGCCCTGGGCCAGCTCTGTCCCACACCGCGGTC  
ACATGGCACCACCTCTCTGACGCTCCACCAAGGGCCCATCCGTCTTCCCC  
TGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCT  
GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCC  
CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTA  
CTCCCTCAGCAGCGTGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC  
TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACA  
GTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTC  
AGCCCTCCTGCGCTGGACGCACCCCGGCTGTGACGCCCCAGCCAGGGCAGCA  
AGGCAGGCCCCATCTGTCTCCTACCCGGAGGCCCTGTGCGCGCCCCACTCATG  
CTCAGGGAGAGGGTCTTCTGGCTTTTCCACCAGGCTCCAGGGAGGCACAGG  
CTGGGTGCCCCCTACCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCA  
GACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCTGACCTAAGCCGACC  
CCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCTCCAGCA  
TCCGAGTAACTCCCAATCTTCTCTCTGACAGCGCAAATGTTGTGTCGAGTGC  
CCACCGTGCCAGGTAAGCCAGGCCAGGCCTCGCCCTCCAGCTCAAGCGGGG  
ACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTG  
ACACGTCCACCTCCATCTCTTCTCAGCACCACCTGTGGCAGGACCGTCAGTC  
TTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCGGGACCCCTGA  
GGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCGAGGTCCAGTTC  
AACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGG  
GAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTCTGC  
ACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG  
GCCTCCCGTCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCA  
CGGGGTGCGAGGGCCACATGGACAGAGGTGAGCTCGGCCCCACCTCTGCCCT  
GGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAGCCA  
CAGGTGTACACCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCA  
GCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTGGAGTG  
GGAGAGCAATGGGCAGCCGGAGAACAATAACAAGACCACGCCTCCCGTGTCT  
GGACTCCGACGGCTCCTTCTTCTCTACAGCAGGCTAACCGTGGACAAGAGC  
AGGTGGCAGGAGGGGAATGTCTTCTCATGTCTCGTGATGCATGAGGCTCTGC  
ACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGTAAATGAGTGCC  
AGGGCCGGCAAGCCCCGCTCCCCGGGCTCTCGGGTTCGCGCGAGGATGCTT  
GGCACGTACCCGCTCTACATACTTCCCAGGCACCCAGCATGGAAATAAAGCA  
CCCACCACTGCCCTGGGCCCCCTGTGAGACTGTGATGGTCTTTCCACGGGTCA  
GGCCGAGTCTGAGGCCTGAGTGACATGAGGAttCAGAtctGGatCC

Bgl II

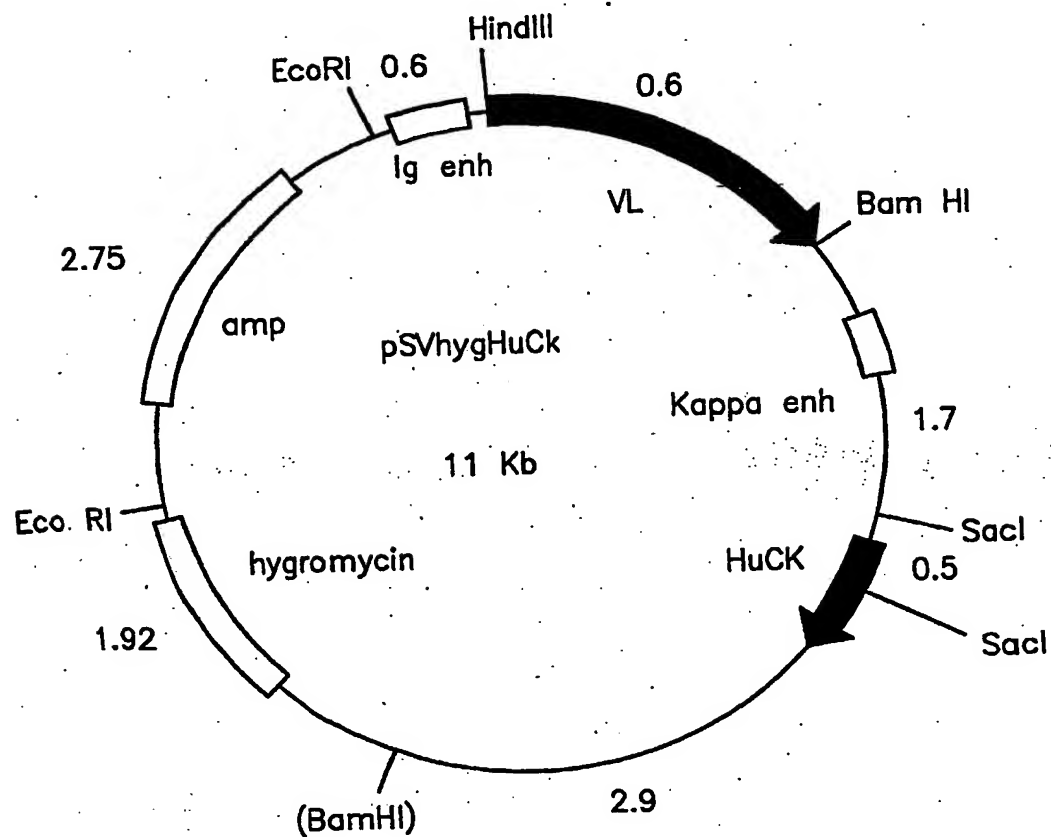
3' untranslated region  
from native IgG4

FIG. 8

SUBSTITUTE SHEET (RULE 26)

22/38

Map of the light chain expression vector pSVgptHuCK

**FIG. 9**

SUBSTITUTE SHEET (RULE 26)

23/38

## Amino Acid sequences of Delimmunised OKT3 heavy chain variable regions

																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					</
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	----

FIG. 10

24/38

61	N	Q	K	F	K	D	K	A	T	L	T	T	D	K	S	S	S	T	A	Y	M	Q	L	S	S	L	T	S	E	D	OKT3 MoVH
61	A	Q	K	F	Q	D	R	V	T	I	T	T	D	K	S	S	S	T	A	Y	L	Q	M	N	S	L	K	T	E	D	OKT3 DIVHv1
61	A	D	S	V	K	G	R	F	T	I	T	T	D	K	S	S	S	T	A	Y	L	Q	M	N	S	L	K	T	E	D	OKT3 DIVHv2
61	N	Q	K	F	K	D	R	V	T	I	T	T	D	K	S	S	S	T	A	Y	L	Q	M	N	S	L	K	T	E	D	OKT3 DIVHv3
61	N	Q	K	V	K	D	R	F	T	I	T	T	D	K	S	S	S	T	A	Y	L	Q	M	N	S	L	K	T	E	D	OKT3 DIVHv4
61	N	Q	K	F	K	D	R	V	T	I	T	T	D	K	S	S	S	T	A	Y	L	Q	M	N	S	L	K	T	E	D	OKT3 DIVHv5
61	A	Q	K	F	Q	D	R	V	T	I	T	T	D	K	S	S	S	T	A	Y	L	Q	M	N	S	L	K	T	E	D	OKT3 DIVHv6
61	N	Q	K	V	K	D	R	F	T	I	T	T	D	K	S	S	S	T	A	Y	L	Q	M	N	S	L	K	T	E	D	OKT3 DIVHv7

91	S	A	V	Y	Y	C	A	R	Y	Y	D	D	H	Y	C	L	D	Y	W	G	Q	G	T	T	L	T	V	S	S	OKT3 MoVH
91	T	A	V	Y	Y	C	A	R	Y	Y	D	D	H	Y	C	L	D	Y	W	G	Q	G	T	T	V	T	V	S	S	OKT3 DIVHv1
91	T	A	V	Y	Y	C	A	R	Y	Y	D	D	H	Y	C	L	D	Y	W	G	Q	G	T	T	V	T	V	S	S	OKT3 DIVHv2
91	T	A	V	Y	Y	C	A	R	Y	Y	D	D	H	Y	C	L	D	Y	W	G	Q	G	T	T	V	T	V	S	S	OKT3 DIVHv3
91	T	A	V	Y	Y	C	A	R	Y	Y	D	D	H	Y	C	L	D	Y	W	G	Q	G	T	T	V	T	V	S	S	OKT3 DIVHv4
91	T	A	V	Y	Y	C	A	R	Y	Y	D	D	H	Y	C	L	D	Y	W	G	Q	G	T	T	V	T	V	S	S	OKT3 DIVHv5
91	T	A	V	Y	Y	C	A	R	Y	Y	D	D	H	Y	C	L	D	Y	W	G	Q	G	T	T	V	T	V	S	S	OKT3 DIVHv6
91	T	A	V	Y	Y	C	A	R	Y	Y	D	D	H	Y	C	L	D	Y	W	G	Q	G	T	T	V	T	V	S	S	OKT3 DIVHv7

FIG. 10 (Cont.)



25/38

## Amino Acid sequences of Delimmunised OKT3 light chain variable regions

(Seq. ID No. 18) {Seq. ID No. 19} {Seq. ID No. 20}	1	Q	I	V	L	T	Q	S	P	A	I	M	S	A	S	P	G	E	K	V	T	M	T	C	S	A	S	S	S	V	S	OKT3 MoVK
	1	Q	I	V	L	T	Q	S	P	A	T	L	S	L	S	P	G	E	R	A	T	L	T	C	S	A	S	S	S	V	S	OKT3 DIVKv1
	1	Q	I	V	L	T	Q	S	P	A	T	L	S	L	S	P	G	E	R	A	T	L	T	C	S	A	S	S	S	V	S	OKT3 DIVKv2
31	31	Y	M	N	W	Y	Q	Q	K	S	G	T	S	P	K	R	W	I	Y	D	T	S	K	L	A	S	G	V	P	A	H	OKT3 MoVK
	31	Y	M	N	W	Y	Q	Q	K	P	G	K	A	P	K	R	W	I	Y	D	T	S	K	L	A	S	G	V	P	S	R	OKT3 DIVKv1
	31	Y	M	N	W	Y	Q	Q	K	P	G	K	A	P	K	R	W	I	Y	D	T	S	K	L	A	S	G	V	P	S	R	OKT3 DIVKv2
61	61	F	R	G	S	G	S	G	T	S	Y	S	L	T	I	S	G	M	E	A	E	D	A	A	T	Y	Y	C	Q	Q	W	OKT3 MoVK
	61	F	S	G	S	G	S	G	T	D	Y	S	L	T	I	N	S	L	E	A	E	D	A	A	T	Y	Y	C	Q	Q	W	OKT3 DIVKv1
	61	F	S	G	S	G	S	G	T	D	Y	S	L	T	I	N	S	L	E	A	E	D	A	A	T	Y	Y	C	Q	Q	W	OKT3 DIVKv2
91	91	S	S	N	P	F	T	F	G	S	G	T	K	L	E	I	N															OKT3 MoVK
	91	S	S	N	P	F	T	F	G	Q	G	T	K	V	E	I	K															OKT3 DIVKv1
	91	S	S	N	P	F	T	F	G	Q	G	T	K	V	E	I	K															OKT3 DIVKv2

FIG. 11

26/38

## OLIGOS FOR CONSTRUCTION OF DIVHs (SEQ ID NOS: 37-57)

KTDIVH1 GAAGTCAAGAAACCTGGGGCCTCAGTGAAGGTGTCCTGCAAGG  
KTDIVH2  
GCCCCAGGTTTCTTGACTTCAGCCCCAGACTGTACCAGCTGGACCTG  
KTDIVH3 TGGGTAAGACAGGCGCCTGGACAAGGTTTGG  
KTDIVH4 GTCCAGGCGCCTGTCTTACCCAGTGCATC  
KTDIVH4A  
AGGCGCCTGTCTTACCCAGTGCATCGTGTACCTAGTAGCCGTGTAGCC  
KTDIVH5 CAATCAGAAGTTCAAGGACAGGGTCACAATCACTACAGACAAA  
KTDIVH5A CGCTCAGAAGTTCCAGGACAGGGTCACAATCACTACAGACAAA  
KTDIVH5B CGCTGACAGTGTCAAGGGCAGGTTCAACAATCACTACAGACAAA  
KTDIVH5C CAATCAGAAGGTCAAGGACAGGTTCAACAATCACTACAGACAAA  
KTDIVH6 GTCCTTGAACCTTCTGATTGTAATTAGTATATCCACGG  
KTDIVH6A GTCCTGGAACCTTCTGAGCGTAATTAGTATATCCACGG  
KTDIVH6B GCCCTTGACACTGTGACGTAATTAGTATATCCACGG  
KTDIVH6C GTCCTTGACCTTCTGATTGTAATTAGTATATCCACGG  
KTDIVH7 AGCCTGAAAACCTGAGGACACCCGAGTCTATTACTG  
KTDIVH8 GTCCTCAGTTTTTCAGGCTGTTTCAATTTGCAAGTAGGCTGTGCT  
KTDIVH9 CCAAGGCACCACTGTGACAGTCTCCTCAGG  
KTDIVH10 CCTGAGGAGACTGTCACAGTGGTGCCTTGG  
KT3VHY GGTGTCCACTCCCAGGTCCAGCTG  
KT3VHZ CAGCTGGACCTGGGAGTGGACACCTGTGG  
VHVK1 GCATGTTGACCCTGACGCAAGCTTATGAATATGCAAA  
VH12 GCGATAGCTGGACTGAATGGATCCTATAAATCTCTG

## OLIGOS FOR CONSTRUCTION OF DIVKs (SEQ ID NOS: 58-74)

KTDIVK1 CCCTCTCTCTTTCTCCAGGGGAACGCGCCACCTTGACATGCAGTG  
KTDIVK2 CCTGGAGAAAGAGAGAGGGTTGCTGGAGACTGGGTG  
KTDIVK3  
CATGAACCTGGTACCAGCAGAAGCCCGGCAAAGCTCCCAAAGATGGAT  
KTDIVK4 CGGGCTTCTGCTGGTACCAGTTCATGTAACCTTACACTT  
KTDIVK4A CTTCTGCTGGTACCAGTTCATGTAACCTTGCACTTGAGC  
KTDIVK5  
GGGTCTGGGACCGATTACTCTCTCACCATCAATAGTCTGGAAGCTGAAG  
KTDIVK6  
GTAATCGGTCCCAGACCCACTGCCACTGAAGCGAGACGGTACTCCAG  
KTDIVK7 TTCACGTTCCGACAAGGTACAAAGGTGGAAATCAAACG  
KTDIVK8 CTTTGTACCTTGTCCGAACGTGAATGGGTTACTTGACC  
KKT22 GCGGATCCAGTCGACGAAGCA  
KT3VKX CTGAATGGATCCAACCTGAGGAAGCAAAGTTTAAATTCTACTCAGG  
KT3VKY CAAATTGTTCTCACCCAGTCTCCAGCAA  
KT3VKZ TTGCTGGAGACTGGGTGAGAACAATTTGGGAG  
KT3VKZ2 TGGAGACTGGGTGAGAACAATTTGGGAGTGGACACCTGTGG  
KT3VKZ3 AGAGAGGGTTGCTGGAGACTGGGTGAGAACAATTTG  
VHVK1 GCATGTTGACCCTGACGCAAGCTTATGAATATGCAAA  
VK12 GCGATAGCTGGACTGAATGGATCCAACCTGAGGAAGC

SUBSTITUTE SHEET (RULE 26)

27/38

## DNA and Amino acid sequence of Delmmunised OKT3 VH version 1.

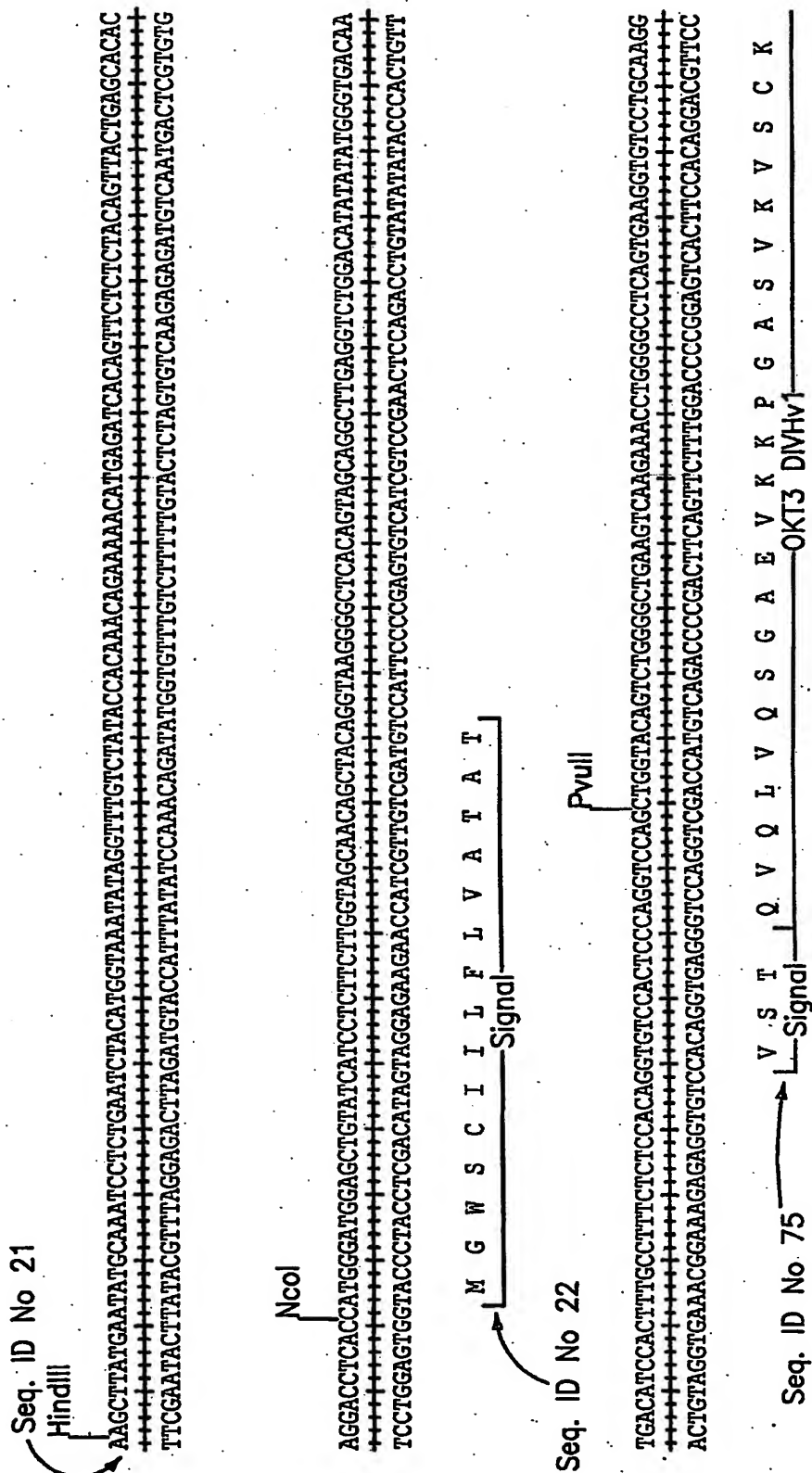


FIG. 13

28/38

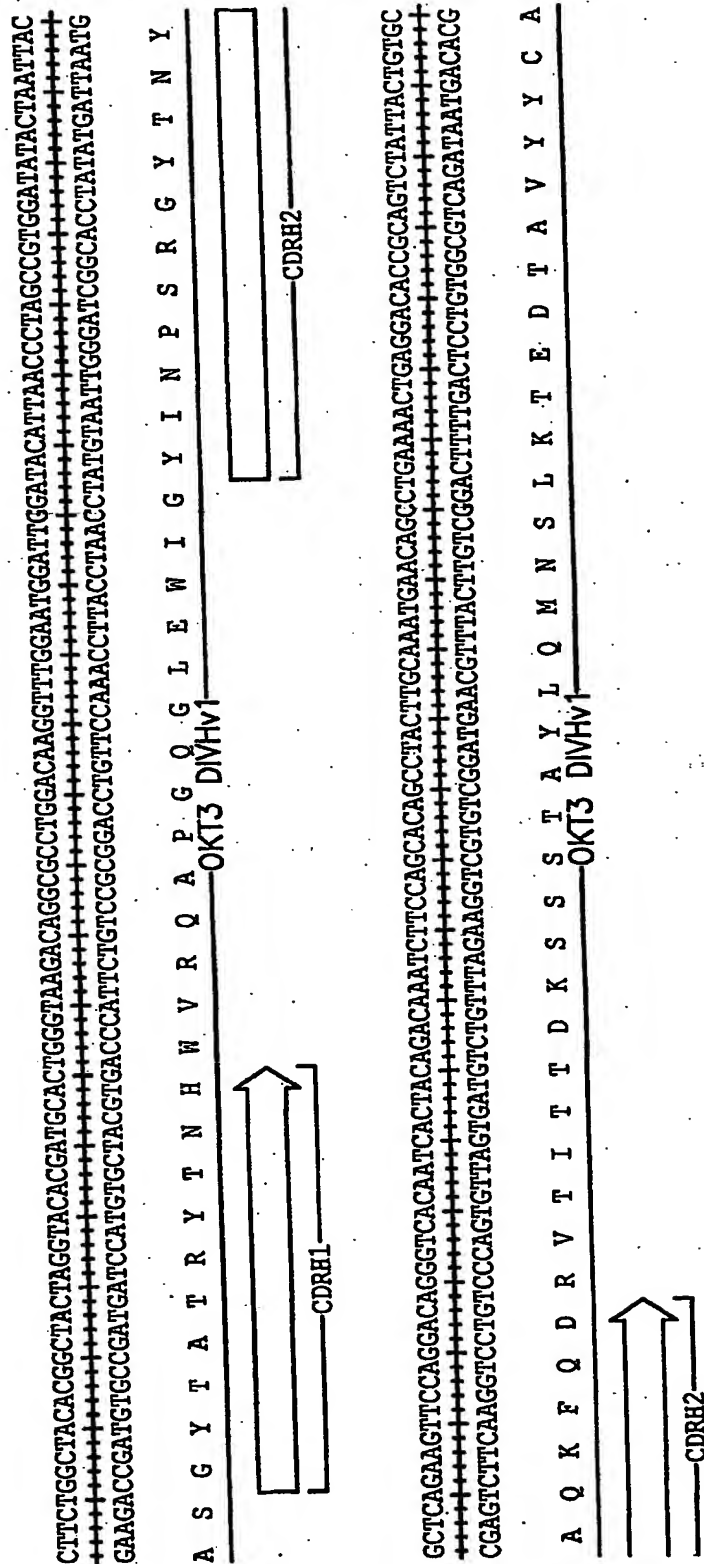
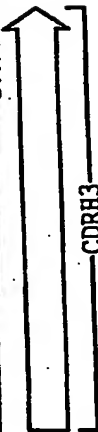


FIG. 13 (Cont.)

29/38

AAGATATTATGATGATCACTACTGTCTCGACTACTGCGGGCCCAAGCACCACCTGTGACAGTCTCTCAGTGAGTCTTACAACCTCTCTCTTCTATTTCAGCTTAAATAGA  
 TTTCTATAATACTACTAGTAATGACAGAGCTGATGACCCCGGTTCCGTGGTGACACTGTTCAGAGGAGTCCACTCAGGAATGTTGGAGAGAGAAAGTAAGTCGAAATTATCT

R Y Y D D H Y C L D Y W G Q G T T V T V S S  
 OKT3 DMHV1



TTTTACTGCAATTTGTGGGGGAAATGTGTGTATCTGTGATTTTCAGGTCAATGAAGACTAGGACACCTTGGGAGTCAGAAAGGTCATTGGGAGCCCGGCTGATCCAG  
 AAAATGACGTAAACAACCCCTTTACACACATAGACTTAAAGTCCAGTACTTCTCTGATCCCTGTGGAACCTCAGTCTTCCAGTAACCTTCGGGCCCCGACTACGTC

XmaI  
SmaI

BamHI

ACAGACATCCTCAGCTCCAGACTTCATGCGCCAGAGATTTATAGGATCC 819  
 TGTCTGAGGAGTCGAGGGTCTGAAGTACCGGTCTCTAAATATCCTAGG

FIG. 13 (Cont.)

30/38

## DNA and Amino Acid Sequence of Delimmunised OKT3 VK version 1.

Seq. ID No 23

HindIII

AAGCTTATGAATATGCAATCCTCTGAATCTACATGGTAAATATAGCTTGTCTATACCAAAACAGAAACATGAGATCACAGTTCTCTACAGTTA  
 ++++++  
 TTCCGAATACTTATACGTTTAGGAGACTTAGATGTACCATTTATATCCAAACAGATATGGTGTCTTTTGTACTCTAGTGTCAAGAGAGATGTCAAT  
 ++++++

NcoI

CTGAGCACACAGGACCTCACCATGGGATGGAGCTGTATCATCTCTTCTGGTAGCAACAGCTACAGGTAGGGGCTCACAGTAGCGTTGAGGCTCTG  
 ++++++  
 GACTCGTGTCTCTGGAGTGTACCTACCTCGACATAGTAGGAGAAGAACCATCGTTGTGATGTCCATTTCCCGAGTGTATCTCGTCCGAACTCCAGAC  
 ++++++

Seq. ID No 24 M G W S C I L L F L V A T A T

Signal

GACATATATGGGTGACAAATGACATCCACTTTGCTCTCCACAGGTGTCCACTCCCAATTTGTTCTCACCCAGTCTCCAGCAACCTCTCTCTTT  
 ++++++  
 CTGTATATATACCCACTGTTACTGTAGGTGAACGGAAAGAGAGGTGTCCACAGGTGAGGTTTAAACAGCTGGGTTCAGAGGTCGTTGGGAGAGAGAAA  
 ++++++

Seq. ID No 76 G V H S Q I V L T Q S P A T L S L

Signal

OKT3 DIVKv1

KpnI

CTCAGGGGAACGGCCACCTTGACATGCCAGTGCAGCTCAAGTGCAGTTACATGACTGGTACAGAGAGCCGGCAAGCTCCCAAAAGATGGAT  
 ++++++  
 GAGGTCCCTTTCGGCGGTGGAACCTGTACGTACGTCGAGTTCAGTTCAGTTCATGACTTGACCATGGTCTCTTCGGGCCCTTCGAGGGTTTCTACCTA  
 ++++++

FIG. 14

31/38

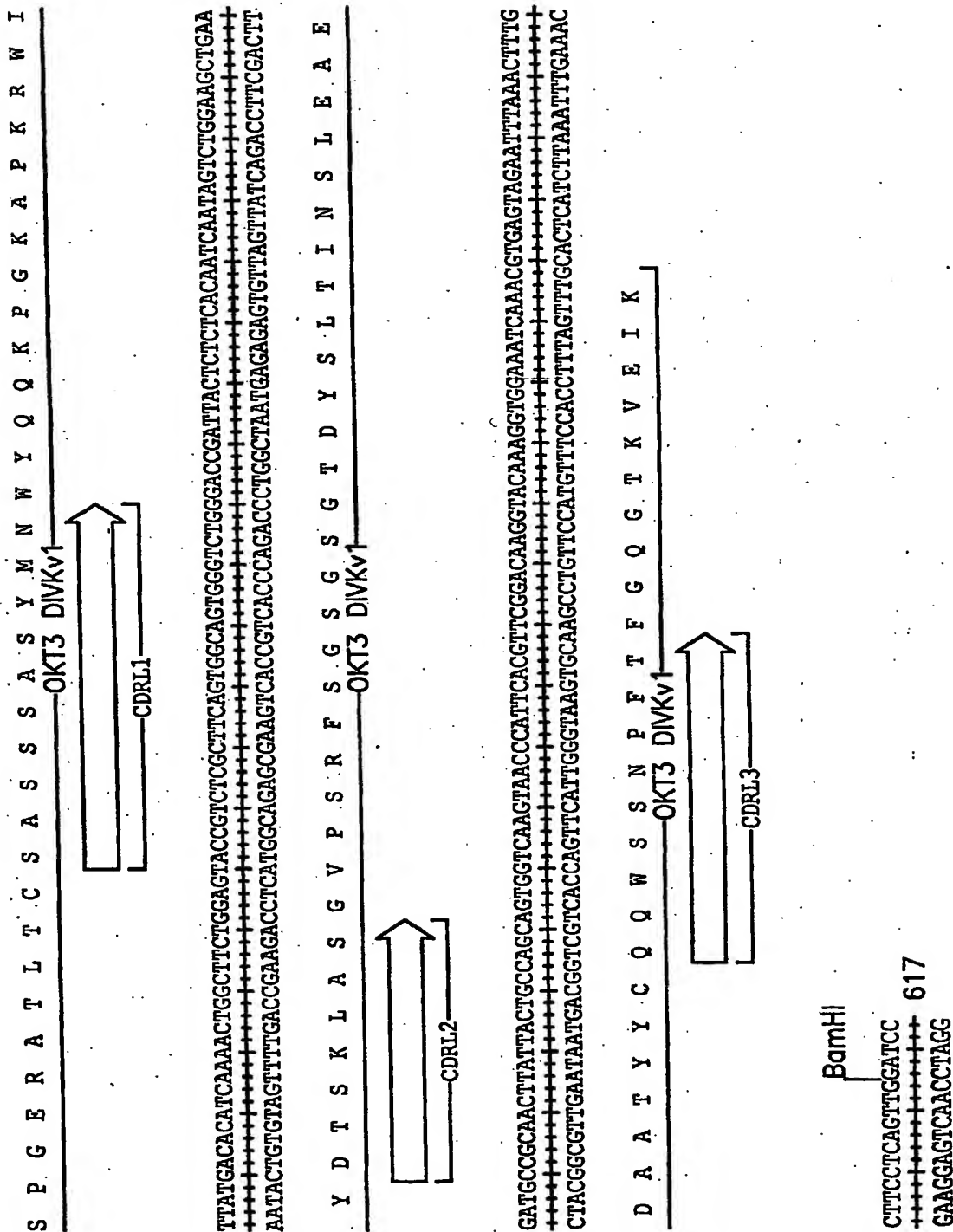


FIG. 14 (Cont.)

32/38

Murine and Chimaeric OKT3 binding to Jurkat, JRT3 and HPB-ALL

cells

Values represent the positive % of gated cells in M1

Cell Type	Passage #	Murine OKT3	Mouse Isotype Control	Chimaeric OKT3	Human Isotype Control
Jurkat	12	81.20	0.5	94.68	0.44
JRT3	14	3.45	0.26	4.56	0.43
HPB-ALL	10	99.63	0.62	99.39	0.29

**FIG. 15**



33/38

Antibody	Clone No.	% Cells in M1	
		HPB-ALL	JRT3
Chimaeric OKT3	N/A	99.74	7.74
Control no OKT3 no PE	N/A	2.22	2.3
Control no OKT3 with PE	N/A	2.3	2.21
DMEM Control	N/A	1.91	2.42
DIVH1/DIVK1	19D6	93.87	2.16
DIVH2/DIVK1	24C12	28.47	2.34
DIVH3/DIVK1	27F6	84.75	2.28
DIVH4/DIVK1	30F7	93.06	2.65
DIVH5/DIVK1	35F2	98.15	2.77
DIVH6/DIVK1	37E9	97.85	3.08
DIVH7/DIVK1	42E7	98.62	3.12

**FIG. 16**

Table 3:

Antibody	Clone No.	% Cells in M1	
		HPB-ALL	JRT3
Chimaeric OKT3	N/A	99.95	0.1
Control no OKT3 no PE	N/A	0.1	0.02
DIVHv1/DIVK2	48G3	20.18	0.1
DIVHv2/DIVK2	52B8	90.04	0.25
DIVHv3/DIVK2	55G5	84.73	0.14
DIVHv4/DIVK2	55B2	69.26	0.13
DIVHv6/DIVK2	66C6	98.16	0.53
DIVHv7/DIVK2	70G10	95.57	0.66

**FIG. 17**

34/38

Competition assay. Inhibition of binding biotinylated mouse OKT3 by chimaeric and Delmmunised OKT3 antibodies, DIVHv1/DIVKv1, DIVHv3/DIVKv1, DIVHv5/DIVKv1, DIVHv6/DIVKv1, OKT3DIVH7/DIVKv1.

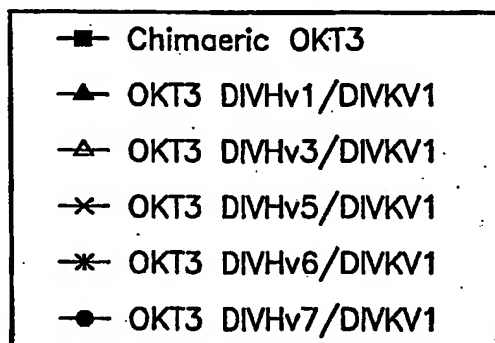
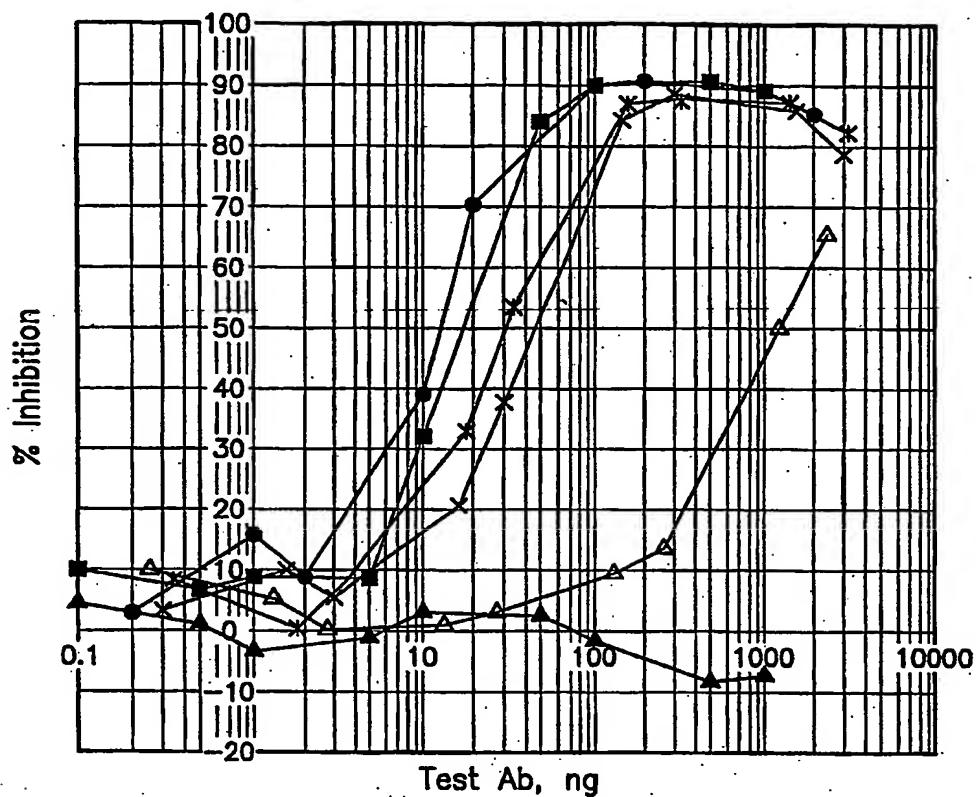
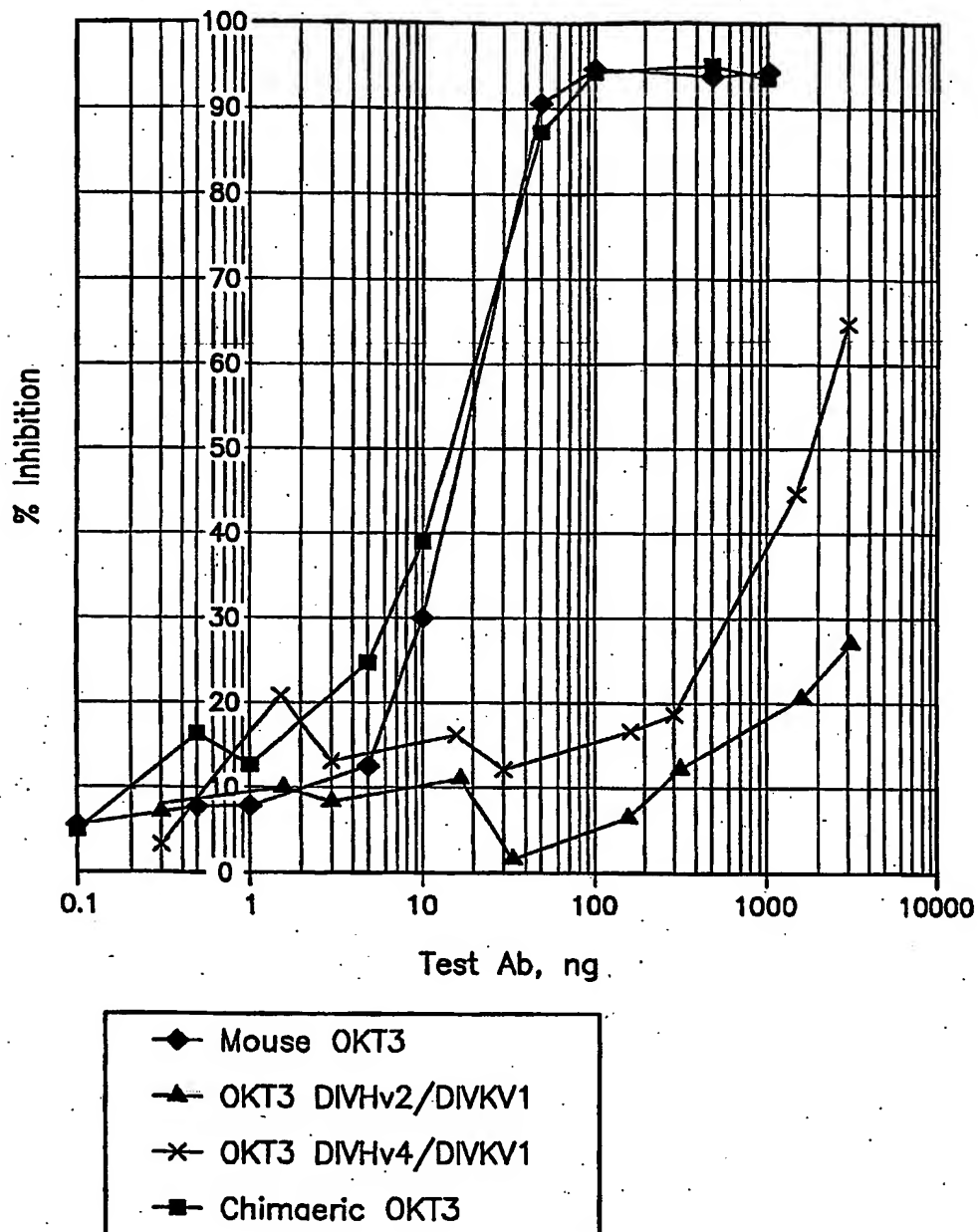


FIG. 18

35/38

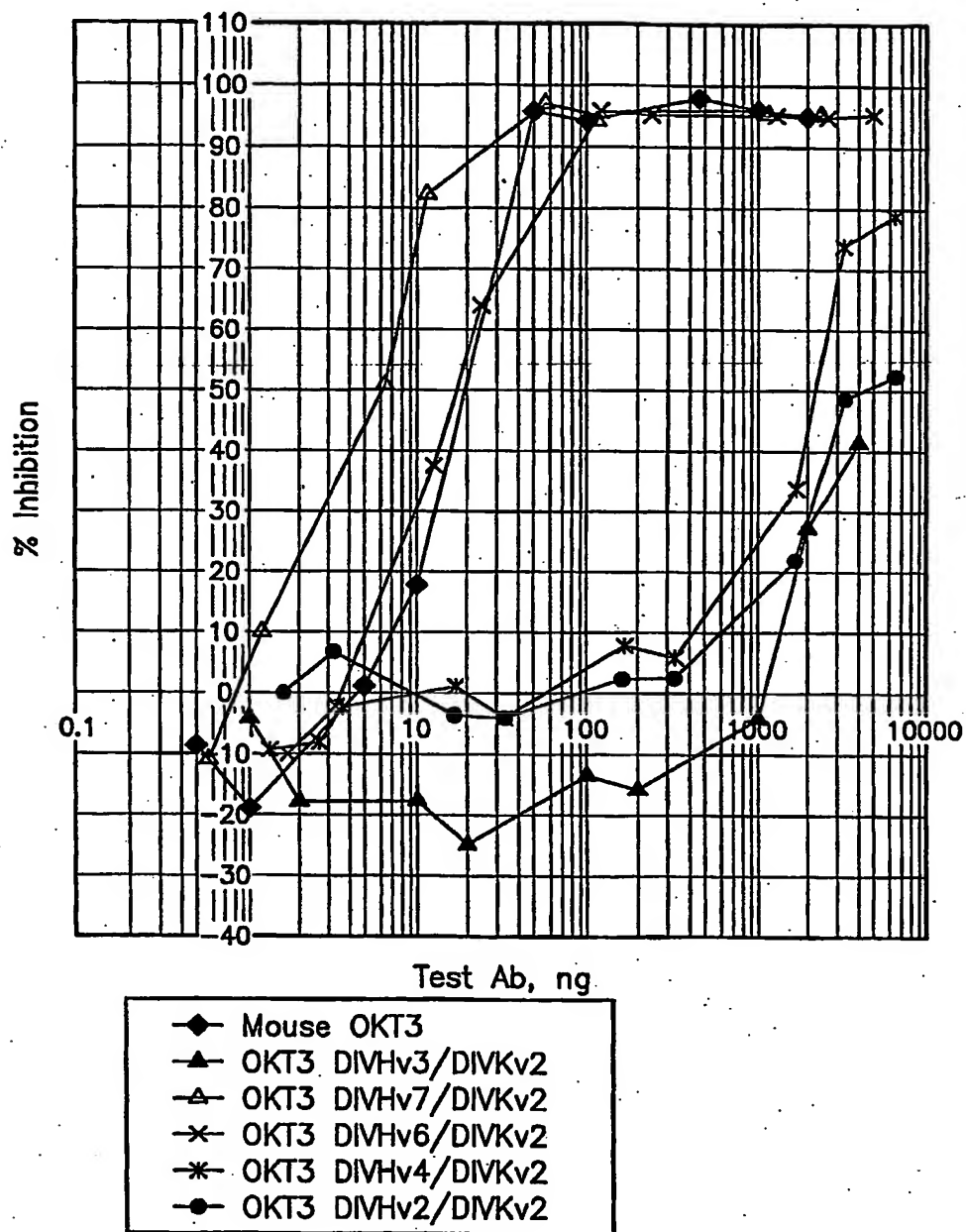
Competition assay. Inhibition of binding biotinylated mouse OKT3 by mouse, chimaeric and Delmmunised OKT3 antibodies DIVHv2/DIVKv1, DIVHv4/DIVKv1.

**FIG. 19**

SUBSTITUTE SHEET (RULE 26)

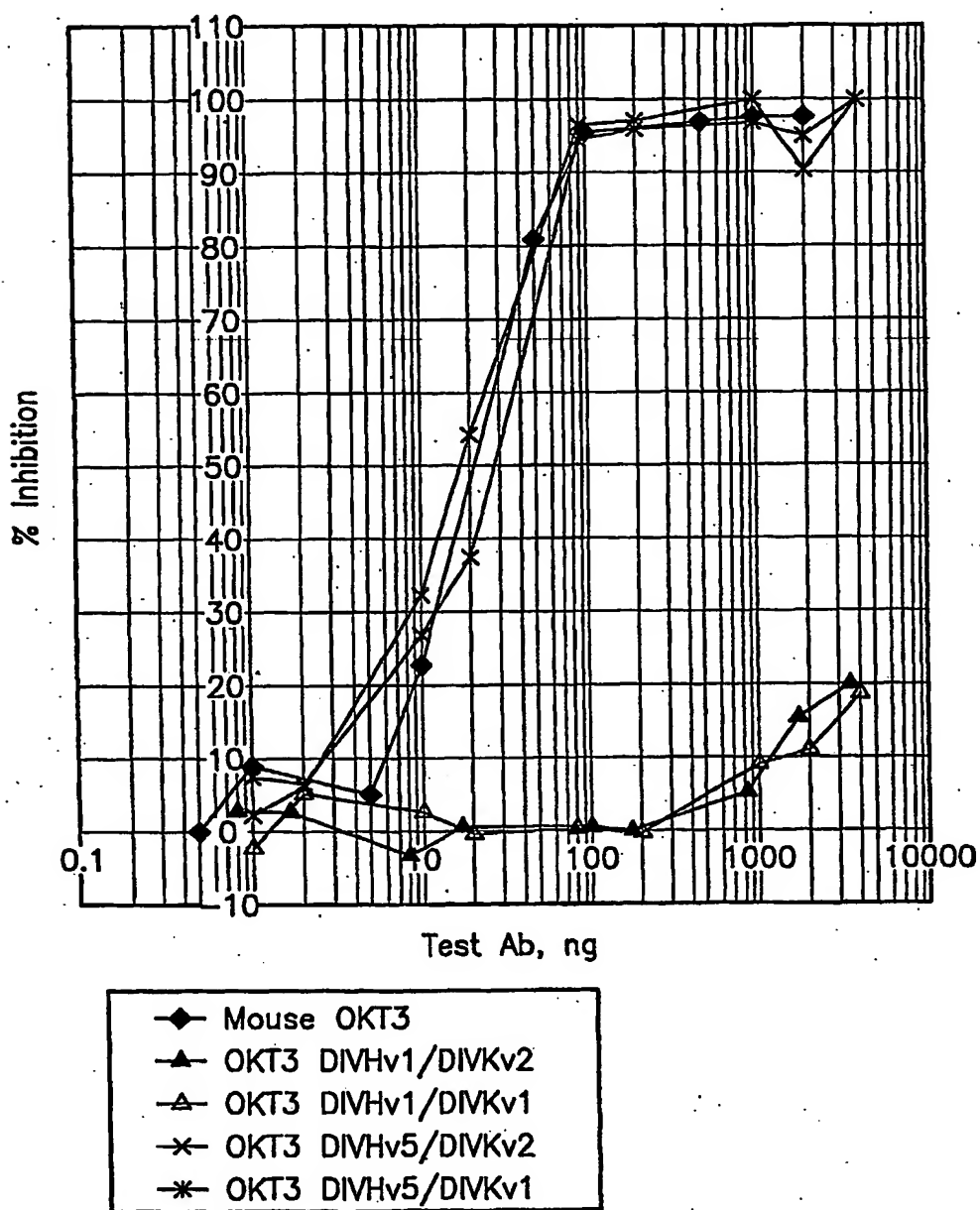
36/38

Competition assay. Inhibition of binding biotinylated mouse OKT3 by mouse, chimaeric and Delmmunised OKT3 antibodies DIVHv3/DIVKv2, DIVHv7/DIVKv2.

**FIG. 20**

37/38

Competition assay. Inhibition of binding biotinylated mouse OKT3 by mouse, chimaeric and Delmmunised OKT3 antibodies DIVHv1/DIVKv2, DIVHv1/DIVKv1, DIVHv5/DIVKv2, DIVHv5/DIVKv1.

**FIG. 21**

38/38

The IC<sub>50</sub> determined from these plots are shown in Table 4.

Table 4:

ANTIBODY	IC <sub>50</sub> (ng)
Murine OKT3 1	18
Murine OKT3 2	19
Murine OKT3 3	20
Chimeric OKT3 1	18
Chimeric OKT3 2	15
De-immunized OKT3 DIVHv1/DIVKv1	N/A
De-imm OKT3 DIVHv1/DIVKv1 2 <sup>nd</sup> prep	>2000
De-immunized OKT3 DIVHv2/DIVKv1	>3000
De-immunized OKT3 DIVHv3/DIVKv1	1250
De-immunized OKT3 DIVHv4/DIVKv1	1900
De-immunized OKT3 DIVHv5/DIVKv1	45
De-imm OKT3 DIVHv5/DIVKv1 2 <sup>nd</sup> prep	19
De-immunized OKT3 DIVHv6/DIVKv1	30
De-immunized OKT3 DIVHv7/DIVKv1	12
De-immunized OKT3 DIVHv1/DIVKv2	>2000
De-immunized OKT3 DIVHv2/DIVKv2	>3000
De-immunized OKT3 DIVHv3/DIVKv2	>4000
De-immunized OKT3 DIVHv4/DIVKv2	2100
De-immunized OKT3 DIVHv5/DIVKv2	28
De-immunized OKT3 DIVHv6/DIVKv2	18
De-immunized OKT3 DIVHv7/DIVKv2	6

**FIG. 22**